What is claimed is:

1. A method of determining the genotype at a locus within genetic material obtained from a biological sample, the method comprising:

A. reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus;

B. forming a data set including the first reaction value;

C. establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

D. applying the first reaction value to each pertinent probability distribution to determine a measure of the conditional probability of each genotype of interest at the locus; and

E. determining the genotype based on the data obtained from step (D).

2. A method according to claim 1, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

3. A method, according to claim 1, further comprising:

(i) reacting the material at the locus to produce a second reaction value independently indicative of the presence of a second allele at the locus;

(ii) forming a second data set including the second reaction value; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

4. A method according to claim 2, further comprising:

(i) reacting the material at the locus to produce a second reaction value;

(ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

5. A method according to claim 3, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

6. A method according to claim 4, wherein each probability distribution associates a hypothetical pair of

first and second reaction values with a single probability of each genotype of interest.

7. A method according to claim 1, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

8. A method according to claim 2, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

9. A method according to claim 3, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions

comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

10. A method according to claim 4, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions; the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values in the first and second data sets.

11. A method, according to claim 7, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(1) performing step (A) with respect to the locus of material obtained from each sample;

(2) in step (B), including in the data set reaction values obtained from each sample.

12. A method according to claim 7, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(1) performing step (A) at each of the selected loci;

(2) in step (B), including in the data set reaction values obtained from each of the selected loci.

13. A method according to claim 7, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

14. A method according to claim 8, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

15. A method according to claim 9, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(2) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(3) using the results of step (2) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

16. A method according to claim 10, wherein step (C) includes:

(1) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

5   (2)   using the initial probability distributions to determine initial conditional probabilities for each genotype at the locus; and

(3)   using the results of step (2) to modify the initial probability distributions, so that the modified

10   distributions more accurately reflect the reaction values in the data.

17.   A method according to claim 13, wherein step (C) further includes:

15   (4) repeating steps (1) through (3) a desired number of times.

18.   A method according to claim 14, wherein step (C) further includes:

20   (4) repeating steps (1) through (3) a desired number of times.

19.   A method according to claim 15, wherein step (C) further includes:

25   (4) repeating steps (1) through (3) a desired number of times.

20.   A method according to claim 16, wherein step (C) further includes:

30   (4) repeating steps (1) through (3) a desired number of times.

21. A method according to claim 1, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

22. A method according to claim 3, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

23. A method according to claim 7, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising (F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

24. A method according to claim 9, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising (F) of determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

25. A method according to claim 1, wherein each allele is a single specific nucleotide.

26. A method according to claim 4, wherein each allele is a single nucleotide.

27. A method according to claim 1, wherein each allele consists of at least two specific nucleotides.

28. A method according to claim 4, wherein each allele consists of at least two specific nucleotides.

29. A method according to claim 1, wherein each allele is defined at least in part by its length in nucleotides.

30. A method according to claim 4, wherein each allele is defined at least in part by its length in nucleotides.

31. A method according to claim 1, wherein each allele is defined by one of the presence and absence of at least one restriction site.

32. A method according to claim 4, wherein each allele is defined by one of the presence and absence of at least one restriction site.
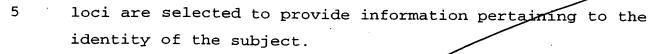
33. A method according to claim 4, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under

5   comparable conditions.

34.   A method according to claim 12, wherein the loci are selected on the basis of their ability to discriminate among subjects.

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35.   A method, according to claim 3, wherein the step A of reacting the material involves using a different reaction from that of step A and the second allele is different from the given allele.

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36.   A method according to claim 1, wherein step (A) includes the step of assaying for the given allele using genetic bit analysis.

20   37.   A method according to claim 1, wherein step (A) includes the step of assaying for the given allele using hybridization.

38.   A method, according to claim 1, wherein step
25   (A) includes the step of assaying for the given allele using allele-specific amplification.

39.   A method, according to claim 1, wherein step
(A) includes the step of assaying for the given allele using
30   a polymerase chain reaction.

40.   A method, according to claim 1, wherein step

(A) includes the step of assaying for the given allele using a ligase chain reaction.

41. A method according to claim 12, wherein the loci are proximal to one another, so that the set of genotypes so produced may indicate a sequence of nucleotides associated with the genetic material.

42. A method of determining the genotype of a subject, the method comprising:

A. reacting genetic material taken from the subject at selected loci, each locus being an identified single nucleotide, to produce with respect to each of the selected loci a reaction value indicative of the presence of a given allele at each of the selected loci;

B. using the reaction values to determine the genotype of the subject and a confidence score, associated with the genotype being determined.

43. A method according to claim 42, wherein the loci are selected to provide information pertaining to inheritance of a trait.

44. A method according to claim 42, wherein the loci are selected to provide information pertaining to parentage of the subject.

45. A method according to claim 42, wherein the

5   loci are selected to provide information pertaining to the
identity of the subject.

46.   A method according to claim 42, wherein the
loci are selected to provide information pertaining to
10   matching tissue of the subject with that of a donor.

47.   A method according to claim 42, wherein the
loci are spaced throughout the entire genome of the subject
to assist in characterizing the genome of the species of the
15   subject.